

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 23, 1999, 22:34:36 ; Search time 360.53 seconds
(without alignments)
38.080 Million cell updates/sec

Title: US-09-205-015-1
Perfect score: 9
Sequence: 1 tctgagtca 9

Scoring table: IDENTITY_NUC

Searched: 2002476 seqs, 762712212 residues

Database : EST.*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: gb_est1:*
11: gb_est2:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: gb_est6:*
16: gb_est7:*
17: gb_est8:*
18: gb_est9:*
19: gb_est10:*
20: gb_est11:*
21: gb_est12:*
22: gb_est13:*
23: gb_est14:*
24: gb_est15:*
25: gb_est16:*
26: gb_est17:*
27: gb_est18:*
28: gb_est19:*
29: gb_est20:*
30: gb_est21:*
31: gb_est22:*
32: em_est10:*
33: em_est11:*
34: em_est12:*
35: em_est13:*
36: em_est14:*
37: em_est15:*
38: em_est16:*
39: em_est17:*
40: em_est18:*
41: em_est19:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	9 100.0	986 10	HSU19036	U19036 Human chrom
2	9 100.0	408 10	M75753	M75753 CEL01A5 Cae

3	9	100.0	542	10	M75778	M75778 CEL02B10 Cae
4	9	100.0	490	10	M75815	M75815 CEL04C3 Cae
5	9	100.0	330	10	M79503	M79503 WEST00040 C
6	9	100.0	411	10	M89881	M89881 CEL12F7 Cae
7	9	100.0	451	10	M89247	M89247 CEL20B1 Cae
8	9	100.0	356	10	M89388	M89388 CEL22B8 Cae
9	9	100.0	434	10	MUSF231A	L26742 Mus musculus
10	9	100.0	436	10	MUSF259A	L26751 Mus musculus
11	9	100.0	496	10	R00048	R00048 ye70e03.s1
12	9	100.0	363	10	R00424	R00424 ye71h05.r1
13	9	100.0	411	10	R01268	R01268 ye81g05.s1
14	9	100.0	397	10	R01396	R01396 ye77a11.s1
15	9	100.0	379	10	R01864	R01864 ye84d12.s1
16	9	100.0	362	10	R02001	R02001 ye82b09.s1
17	9	100.0	422	10	R02139	R02139 ye87a01.s1
18	9	100.0	350	10	R03267	R03267 pk05e04.s1
19	9	100.0	376	10	R04520	R04520 pk24g01.s1
20	9	100.0	389	10	R05588	R05588 ye92a02.r1
21	9	100.0	278	10	R05679	R05679 yf12b05.r1
22	9	100.0	501	10	R06930	R06930 yf12b05.r1
23	9	100.0	440	10	R07369	R07369 ye96h06.s1
24	9	100.0	298	10	R08467	R08467 ye95b01.r1
25	9	100.0	428	10	R08746	R08746 yf20a11.s1
26	9	100.0	384	10	R08764	R08764 yf20d10.s1
27	9	100.0	241	10	R08849	R08849 yf21b08.s1
28	9	100.0	369	10	R09135	R09135 yf25f10.r1
29	9	100.0	421	10	R09518	R09518 yf27a04.s1
30	9	100.0	389	10	R09829	R09829 yf30a09.r1
31	9	100.0	466	10	R10075	R10075 yf35b02.s1
32	9	100.0	351	10	R10086	R10086 yf35c07.s1
33	9	100.0	337	10	R10246	R10246 yf32e07.r1
34	9	100.0	444	10	R10424	R10424 yf28f09.r1
35	9	100.0	403	10	R11110	R11110 yf39f01.r1
36	9	100.0	294	10	R11613	R11613 yf47e11.r1
37	9	100.0	457	10	R11682	R11682 yf49a07.r1
38	9	100.0	371	10	R12038	R12038 yf53e09.r1
39	9	100.0	391	10	R12308	R12308 yf55b02.r1
40	9	100.0	368	10	R12822	R12822 yf57c11.r1
41	9	100.0	407	10	R13319	R13319 yf75f03.r1
42	9	100.0	455	10	R13924	R13924 yf62f05.r1
43	9	100.0	404	10	R14091	R14091 yf69a08.r1
44	9	100.0	447	10	R14267	R14267 yf79e05.r1
45	9	100.0	587	31	C98064	C98064 Oryza sativ

ALIGNMENTS

RESULT 1

HSU19036 986 bp mRNA EST 09-MAR-1995
LOCUS Human chromosome 5q12 clone XS2G3 mRNA, 3' UTR.
DEFINITION
ACCESSION U19036
NID 9643632
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 980)
Thompson,T.G., DiDonato,C.J., Simard,L.R., Ingram,S.E., Burghes,A.H.-N., Crawford,T.O., Rochette,C., Mendell,J.R. and Wasmuth,J.J.

A novel cDNA detects homozygous microdeletions in greater than 50% of type I spinal muscular atrophy patients
Nature Genet. 9, 56-62 (1995)
2 (bases 1 to 980)
Thompson,T.G.
Direct Submission

JOURNAL

Submitted (22-DEC-1994) Terri G. Thompson, Biological Chemistry, University of California at Irvine, D240, Med Sci I, University of California at Irvine, Irvine, CA 92717, USA
On Feb 8, 1995 this sequence version replaced gi:642020.

FEATURES	source	Location/Qualifiers
LOCUS	M75778	542 bp mRNA EST 16-SEP-1992
DEFINITION	CEL02B10	Caenorhabditis elegans cDNA clone cm02b10 5'
ACCESSION	M75778	
NID	9275128	
KEYWORDS	EST.	
SOURCE		Nematodes clone-cm02b10 library=Chris Martin sorted cDNA library strain-Bristol N2 vector-lambda phage SHLX2 host-MC1061 Mixed stage hermaphrodite cDNA library. Partially normalized by successively picking groups of clones that didn't hybridize to previously picked clones. Vector: lambda phage SHLX2 (Lipshitz, D.H. et al., Gene 88:25-36 (1990)). Host: MC1061.
ORGANISM		Caenorhabditis elegans
REFERENCE		Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae.
AUTHORS		Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A., Hillier,L., Durbin,R.K., Green,P., Showkneen,R., Halloran,N., Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J. and Sulston,J.
TITLE		A survey of expressed genes in Caenorhabditis elegans
JOURNAL		Nature Genet. 1, 114-123 (1992)
COMMENT		Contact: Waterston R.H.(USA) and Sulston J.E.(UK) (USA) Dept. of Genetics or (UK) (USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of Molecular Biology Box 8232,4566 Scott Ave., St. Louis,MI 63110,USA,or,Hills Road,Cambridge CB2 2QH,UK Tel: (USA) (314)3627072 or (UK) (0223)248011 Fax: (USA) (314)3624137 or (UK) (0223)402008 Email: rwnematode.wustl.edu or jesemrc-lmb.cam.ac.uk.
FEATURES		Location/Qualifiers
Source		1..542
		/organism="Caenorhabditis elegans"
		/clone="cm02b10"
		/strain="Bristol N2"
BASE COUNT	160 a	100 c 145 g 128 t 9 others
ORIGIN		
Query Match		100.0%; Score 9; DB 10; Length 542;
Best Local Similarity		100.0%; Pred. No. 6.1e+03;
Matches	9; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	tctgagtcga 9
DB	88	TCTGAGTCA 96
RESULT	4	
LOCUS	M75815	490 bp mRNA EST 15-SEP-1992
DEFINITION	CEL04C3	Caenorhabditis elegans cDNA clone cm04c3 5'
ACCESSION	M75815	
NID	9275168	
KEYWORDS	EST.	
SOURCE		Nematodes clone-cm04c3 library=Chris Martin sorted cDNA library strain-Bristol N2 vector-lambda phage SHLX2 host-MC1061 Mixed stage hermaphrodite cDNA library. Partially normalized by successively picking groups of clones that didn't hybridize to previously picked clones. Vector: lambda phage SHLX2 (Lipshitz, D.H. et al., Gene 88:25-36 (1990)). Host: MC1061.
ORGANISM		Caenorhabditis elegans
REFERENCE		Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae.
AUTHORS		Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A., Hillier,L., Durbin,R.K., Green,P., Showkneen,R., Halloran,N., Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J. and Sulston,J.
TITLE		A survey of expressed genes in Caenorhabditis elegans
JOURNAL		Nature Genet. 1, 114-123 (1992)
COMMENT		Contact: Waterston R.H.(USA) and Sulston J.E.(UK) (USA) Dept. of Genetics or (UK) (USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of Molecular Biology Box 8232,4566 Scott Ave., St. Louis,MI 63110,USA,or,Hills Road,Cambridge CB2 2QH,UK Tel: (USA) (314)3627072 or (UK) (0223)248011 Fax: (USA) (314)3624137 or (UK) (0223)402008 Email: rwnematode.wustl.edu or jesemrc-lmb.cam.ac.uk.
FEATURES		Location/Qualifiers
Source		1..408
		/organism="Caenorhabditis elegans"
		/clone="cm01a5"
		/strain="Bristol N2"
BASE COUNT	115 a	89 c 97 g 102 t 5 others
ORIGIN		
Query Match		100.0%; Score 9; DB 10; Length 408;
Best Local Similarity		100.0%; Pred. No. 6.1e+03;
Matches	9; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	tctgagtcga 9
DB	144	TCTGAGTCA 136

JOURNAL COMMENT

Nature Genet. 1, 114-123 (1992)

Contact: Waterston R.H.(USA) and Sulston J.E.(UK)
(USA) Dept. of Genetics or (UK)
(USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of
Molecular Biology
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Road,Cambridge CB2 2QH,UK
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Fax: (USA) (314)3624137 or (UK) (0223)402008
Email: rw@nematode.wustl.edu or jes@mrc-lmb.cam.ac.uk.

FEATURES

source

1..490
/organism="Caenorhabditis elegans"
/clone="cm04c3"
/strain="Bristol N2"

BASE COUNT 135 a 100 c 111 g 141 t 3 others

ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 490;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
|||||

Db 61 TCTGAGTCA 69

RESULT 5

M79503/c

LOCUS

DEFINITION M79503 330 bp mRNA EST 30-JUN-1992

ACCESSION WEST00040 Caenorhabditis elegans cDNA clone CEMSA23 similar to

NID Tropomyosin.

KEYWORDS

SOURCE M79503

ORGANISM

Caenorhabditis elegans

REFERENCE

AUTHORS

McCombie,W.R., Adams,M.D., Kelley,J.M., FitzGerald,M.G.,
Utterback,T.R., Khan,M., Dubnick,M., Kerlavage,A.R., Venter,J. and
Fields,C.

TITLE

Caenorhabditis elegans expressed sequence tags reveal gene families
and potential disease gene homologues

JOURNAL

COMMENT

Nature Genet. 1, 124-131 (1992)

*Other_ESTs: WEST00039

Contact: Kerlavage AR
The Institute for Genomic Research
932 Clopper Road,Gaithersburg,MD 20878
Tel: 3018690056
Fax: 301869423
Email: arkerl@vetigr.org.

FEATURES

source

1..330
Location/Qualifiers
/organism="Caenorhabditis elegans"
/clone="CEMSA23"

BASE COUNT 100 a 74 c 88 g 52 t 6 others

ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 330;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
|||||

Db 188 TCTGAGTCA 180

RESULT 6

M88981/c

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

SOURCE

M88981

EST

411 bp mRNA

EST

02-DEC-1992

CDNA clone cm12f7 5' similar to

Ca2+-transporting ATPase homologous peptide.

M88981

EST

Nematodes clone-cm12f7 library=Chris Martin sorted cDNA library

strain-Bristol N2 vector-lambda phage SHLX2 host-MC1061 Mixed stage

hermaphrodite cDNA library. Partially normalized by successively

picking groups of clones that didn't hybridize to previously picked

clones. Vector: lambda phage SHLX2 (Lipshitz, D.H. et al., Gene

88:25-36 (1990)) Host: MC1061.

Caenorhabditis elegans

Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae.

1 (bases 1 to 411)

Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A.,

Hillier,L., Durbin,R.K., Green,P., Shownkeen,R., Halloran,N.,

Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J.

and Sulston J.

A survey of expressed genes in Caenorhabditis elegans

Nature Genet. 1, 114-123 (1992)

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Email: rw@nematode.wustl.edu or jes@mrc-lmb.cam.ac.uk.

Location/Qualifiers

1..411

/organism="Caenorhabditis elegans"

/clone="cm12f7"

/strain="Bristol N2"

120 a 85 c 97 g 105 t 4 others

BASE COUNT

ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 411;

Best Local Similarity 100.0%; Pred. No. 6.1e+03;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9

|||||

Db 121 TCTGAGTCA 113

RESULT 7

M89247/c

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

SOURCE

M89247

EST

461 bp mRNA

EST

02-DEC-1992

CDNA clone cm20b1 5' similar to

Ca2+-transporting ATPase homologous peptide.

M89247

EST

Nematodes clone-cm20b1 library=Chris Martin sorted cDNA library

strain-Bristol N2 vector-lambda phage SHLX2 host-MC1061 Mixed stage

hermaphrodite cDNA library. Partially normalized by successively

picking groups of clones that didn't hybridize to previously picked

clones. Vector: lambda phage SHLX2 (Lipshitz, D.H. et al., Gene

88:25-36 (1990)) Host: MC1061.

Caenorhabditis elegans

Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae.

1 (bases 1 to 461)

Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A.,

Hillier, L., Durbin, R.K., Green, P., Shownkeen, R., Halloran, N.,
Hawkins, T., Wilson, R., Berks, M., Du, Z., Thomas, K., Thierry-Mieg, J.,
and Sulston, J.
A survey of expressed genes in *Caenorhabditis elegans*
Nature Genet. 1, 114-123 (1992)

COMMENT

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Tel: (USA) (314) 3624137 or (UK) (0223) 402008
Fax: (USA) (314) 3624137 or (UK) (0223) 402008
Email: rwenematode.wustl.edu or jes@ncrc-lmb.cam.ac.uk.

FEATURES

source

1. .461
/organism="Caenorhabditis elegans"
/clone="cm20b1"
/strain="Bristol N2"

BASE COUNT 136 a 120 c 109 g 94 t 2 others

ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9

Db 67 TCTGAGTCA 59

RESULT

M89388/c

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

SOURCE

M89388 356 bp mRNA EST 16-SEP-1992
CEL22E8 *Caenorhabditis elegans* cDNA clone cm22e8 5'.

M89388

9275893

EST

Nematodes clone-cm22e8 library-Chris Martin sorted cDNA library
strain-Bristol N2 vector-lambda phage SHLX2 host-MC1061 Mixed stage
hermaphrodite cDNA library. Partially normalized by successively
picking groups of clones that didn't hybridize to previously picked
clones. Vector: lambda phage SHLX2 (Lipshitz, D.H. et al., Gene
88:25-36 (1990)). Host: MC1061.

Caenorhabditis elegans

Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae.

1 (bases 1 to 356)

Waterston, R., Martin, C., Craxton, M., Huynh, C., Coulson, A.,
Hillier, L., Durbin, R.K., Green, P., Shownkeen, R., Halloran, N.,
Hawkins, T., Wilson, R., Berks, M., Du, Z., Thomas, K., Thierry-Mieg, J.,
and Sulston, J.

A survey of expressed genes in *Caenorhabditis elegans*

Nature Genet. 1, 114-123 (1992)

TITLE

JOURNAL

COMMENT

Contact: Waterston R.H.(USA) and Sulston J.E.(UK)
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(USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of
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Fax: (USA) (314) 3624137 or (UK) (0223) 402008

Email: rwenematode.wustl.edu or jes@ncrc-lmb.cam.ac.uk.

Location/Qualifiers

1. .356

/organism="Caenorhabditis elegans"

/clone="cm22e8"

/strain="Bristol N2"

BASE COUNT 110 a 62 c 80 g 102 t 2 others

ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 356;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9

Db 294 TCTGAGTCA 286

RESULT

MUSF231A

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

SOURCE

MUSF231A 434 bp mRNA EST 24-FEB-1995
Mus musculus expressed sequence tag EST F231, mRNA sequence.

L26742

9437523

EST; expressed sequence tag.

Mus musculus (strain Swiss)

testis cDNA to mRNA.

ORGANISM

Mus musculus

Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae;

Murinae; Mus.

1 (bases 1 to 434)

Kerr, S.M., Vambrie, S., McKay, S.J. and Cooke, H.J.

Analysis of cDNA sequences from mouse testis

Mamm. Genome 5 (9), 557-565 (1994)

MEDLINE

95093181

FEATURES

Location/Qualifiers

1. .434

/organism="Mus musculus"

/strain="Swiss"

/db_xref="taxon:10090"

/sex="male"

/tissue_type="testis"

/tissue_lib="lambda unizap"

BASE COUNT 133 a 82 c 64 g 154 t

ORIGIN

1 others

Query Match 100.0%; Score 9; DB 10; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9

Db 280 TCTGAGTCA 288

RESULT

MUSF259A/c

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

SOURCE

MUSF259A 436 bp mRNA EST 24-FEB-1995
Mus musculus expressed sequence tag EST F259, mRNA sequence.

L26751

9437531

EST; expressed sequence tag.

Mus musculus (strain Swiss)

testis cDNA to mRNA.

ORGANISM

Mus musculus

Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae;

Murinae; Mus.

1 (bases 1 to 436)

Kerr, S.M., Vambrie, S., McKay, S.J. and Cooke, H.J.

Analysis of cDNA sequences from mouse testis

Mamm. Genome 5 (9), 557-565 (1994)

MEDLINE

95093181

FEATURES

Location/Qualifiers

1. .436

/organism="Mus musculus"

/strain="Swiss"

/db_xref="taxon:10090"

```

/sex="male"
/tissue_type="testis"
/tissue_lib="lambda unizap"
BASE COUNT      131 a      76 c      112 g      116 t      1 others
ORIGIN

Query Match      100.0%; Score 9; DB 10; Length 436;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9
|||||
Db 202 TCTGAGTCA 194

RESULT 11
R00048
LOCUS      496 bp      mRNA      EST      31-MAR-1995
DEFINITION      ye70e03.s1 Homo sapiens cDNA clone 123100 3'.
ACCESSION      R00048
NID      9749784
KEYWORDS
SOURCE
human clone=123100 library=Soares fetal liver spleen lNFLS
vector=PT73D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=21m13 Rsite1-Pac I Rsite2-Eco RI
Liver and spleen from a 20 week-post conception male fetus. 1st
strand cDNA was primed with a Pac I - oligo(dT) primer [5',
AACTGGAAGATTAATAAGATCTTTTCTTTTCTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM      Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 496)
REFERENCE
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 393
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source
1..496
/organism="Homo sapiens"
/clone="123100"
BASE COUNT      116 a      126 c      125 g      126 t      3 others
ORIGIN

Query Match      100.0%; Score 9; DB 10; Length 496;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9
|||||
Db 334 TCTGAGTCA 342

RESULT 12
R00424
LOCUS      363 bp      mRNA      EST      31-MAR-1995
DEFINITION      ye71h05.r1 Homo sapiens cDNA clone 123225 5'.
ACCESSION      R00424
NID      9750160
KEYWORDS
SOURCE
human clone=123225 library=Soares fetal liver spleen lNFLS
vector=PT73D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=M13RPI Rsite1-Pac I Rsite2-Eco RI
Liver and spleen from a 20 week-post conception male fetus. 1st
strand cDNA was primed with a Pac I - oligo(dT) primer [5',
AACTGGAAGATTAATAAGATCTTTTCTTTTCTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM      Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 363)
REFERENCE
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 202
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source
1..363
/organism="Homo sapiens"
/clone="123225"
BASE COUNT      91 a      93 c      97 g      78 t      4 others
ORIGIN

Query Match      100.0%; Score 9; DB 10; Length 363;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9
|||||
Db 112 TCTGAGTCA 120

RESULT 13
R01268/c
LOCUS      411 bp      mRNA      EST      31-MAR-1995
DEFINITION      ye81g05.s1 Homo sapiens cDNA clone 124184 3'.
ACCESSION      R01268
NID      9751004
KEYWORDS
SOURCE
human clone=124184 library=Soares fetal liver spleen lNFLS
vector=PT73D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=21m13 Rsite1-Pac I Rsite2-Eco RI
Liver and spleen from a 20 week-post conception male fetus. 1st
strand cDNA was primed with a Pac I - oligo(dT) primer [5',
AACTGGAAGATTAATAAGATCTTTTCTTTTCTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library

```

ORGANISM	constructed by Bento Soares and M.Fatima Bonaído.
REFERENCE	Homo sapiens Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 411)
AUTHORS	Elliston, K., Hawkins, M., Hillman, L., Clark, N., Dubucque, T., Holter, M., Hultman, M., Kucaba, T., Parsons, J., Rifkin, L., Rohlfing, T., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)

FEATURES	Location/Qualifiers	Score	DB	Length
source	1..411	100.0%	9	411
	/organism="Homo sapiens"	100.0%		
	/clone="124134"			
BASE COUNT	121 a 75 c 122 g 89 t 4 others			
ORIGIN				
Query Match		100.0%	Score 9	DB 10
Best Local Similarity		100.0%	Pred. No. 6.1e-03	
Method				
9. Conservative		0	Mismatches	0
			Indels	0
			Gaps	0

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES	Location/Qualifiers
source	1. .397 /organism="Homo sapiens" /clone="123740"
BASE COUNT	94 a 96 c 90 g 115 t
ORIGIN	2 others

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Query Match      100.0%; Score 9; DB 10; Length 397;
Best Local Similarity 100.0%; Pred. No. 6.1e-03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 tctgagagtca 9
          |||||
Db       327 TCTGAGTCA 319

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TITLE
The WashU-Merck EST Project
JOURNAL
Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project

Query Match 100.0%; Score 9; DB 10; Length 379;
Best Local Similarity 100.0%; Pred. No. 6.le-03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tctgagtca 9
| | | | | | | | | |
Db 163 TCTGAGTCA 155

Search completed: June 23, 1999, 23:01:43
Job time: 1627 sec

